

Range : 1 - 1053 Mode : Normal

Codon Table : Universal

9	18	27	36	45	54
5' ATG GGC GAC CCG GAA AGG CCG GAA GCG GCC GGG CTG GAT CAG GAT GAG AGA TCA					
Met Gly Asp Pro Glu Arg Pro Glu Ala Ala Gly Leu Asp Gln Asp Glu Arg Ser					
63	72	81	90	99	108
TCT TCA GAC ACC AAC GAA AGT GAA ATA AAG TCA AAT GAA GAG CCA CTC CTA AGA					
Ser Ser Asp Thr Asn Glu Ser Glu Ile Lys Ser Asn Glu Glu Pro Leu Leu Arg					
117	126	135	144	153	162
AAG AGT TCT CGC CGG TTT GTC ATC TTT CCA ATC CAG TAC CCT GAT ATT TGG AAA					
Lys Ser Ser Arg Arg Phe Val Ile Phe Pro Ile Gln Tyr Pro Asp Ile Trp Lys					
171	180	189	198	207	216
ATG TAT AAA CAG GCA CAG GCT TCC TTC TGG ACA GCA GAA GAG GTC GAC TTA TCA					
Met Tyr Lys Gln Ala Gln Ala Ser Phe Trp Thr Ala Glu Glu Val Asp Leu Ser					
225	234	243	252	261	270
AAG GAT CTC CCT CAC TGG AAC AAG CTT AAA GCA GAT GAG AAG TAC TTC ATC TCT					
Lys Asp Leu Pro His Trp Asn Lys Leu Lys Ala Asp Glu Lys Tyr Phe Ile Ser					
279	288	297	306	315	324
CAC ATC TTA GCC TTT TTT GCA GCC AGT GAT GGA ATT GTA AAT GAA AAT TTG GTG					
His Ile Leu Ala Phe Phe Ala Ala Ser Asp Gly Ile Val Asn Glu Asn Leu Val					
333	342	351	360	369	378
GAG CGC TTT AGT CAG GAG GTG CAG GTT CCA GAG GCT CGC TGT TTC TAT GGC TTT					
Glu Arg Phe Ser Gln Glu Val Gln Val Pro Glu Ala Arg Cys Phe Tyr Gly Phe					
387	396	405	414	423	432
CAA ATT CTC ATC GAG AAT GTT CAC TCA GAG ATG TAC AGT TTG CTG ATA GAC ACT					
Gln Ile Leu Ile Glu Asn Val His Ser Glu Met Tyr Ser Leu Leu Ile Asp Thr					

441	450	459	468	477	486
TAC ATC AGA GAT CCC AAG AAA AGG GAA TTT TTA TTT AAT GCA ATT GAA ACC ATG					
Tyr Ile Arg Asp Pro Lys Lys Arg Glu Phe Leu Phe Asn Ala Ile Glu Thr Met					

495	504	513	522	531	540
CCC TAT GTT AAG AAA AAA GCA GAT TGG GCC TTG CGA TGG ATA GCA GAT AGA AAA					
Pro Tyr Val Lys Lys Lys Ala Asp Trp Ala Leu Arg Trp Ile Ala Asp Arg Lys					

549	558	567	576	585	594
TCT ACT TTT GGG GAA AGA GTG GTG GCC TTT GCT GCT GTA GAA GGA GTT TTC TTC					
Ser Thr Phe Gly Glu Arg Val Val Ala Phe Ala Ala Val Glu Gly Val Phe Phe					

603	612	621	630	639	648
TCA GGA TCT TTT GCT GCT ATA TTC TGG CTA AAG AAG AGA GGT CTT ATG CCA GGA					
Ser Gly Ser Phe Ala Ala Ile Phe Trp Leu Lys Lys Arg Gly Leu Met Pro Gly					

657	666	675	684	693	702
CTC ACT TTT TCC AAT GAA CTC ATC AGC AGA GAT GAA GGA CTT CAC TGT GAC TTT					
Leu Thr Phe Ser Asn Glu Leu Ile Ser Arg Asp Glu Gly Leu His Cys Asp Phe					

711	720	729	738	747	756
GCT TGC CTG ATG TTC CAA TAC TTA GTA AAT AAG CCT TCA GAA GAA AGG GTC AGG					
Ala Cys Leu Met Phe Gln Tyr Leu Val Asn Lys Pro Ser Glu Glu Arg Val Arg					

765	774	783	792	801	810
GAG ATC ATT GTT GAT GCT GTC AAA ATT GAG CAG GAG TTT TTA ACA GAA GCC TTG					
Glu Ile Ile Val Asp Ala Val Lys Ile Glu Gln Glu Phe Leu Thr Glu Ala Leu					

819	828	837	846	855	864
CCA GTT GGC CTC ATT GGA ATG AAT TGC ATT TTG ATG AAA CAG TAC ATT GAG TTT					
Pro Val Gly Leu Ile Gly Met Asn Cys Ile Leu Met Lys Gln Tyr Ile Glu Phe					

873	882	891	900	909	918
GTA GCT GAC AGA TTA CTT GTG GAA CTT GGA TTC TCA AAG GTT TTT CAG GCA GAA					
Val Ala Asp Arg Leu Leu Val Glu Leu Gly Phe Ser Lys Val Phe Gln Ala Glu					

FIG. 2

927	936	945	954	963	972
AAT CCT TTT GAT TTT ATG GAA AAC ATT TCT TTA GAA GGA AAA ACA AAT TTC TTT					

Asn Pro Phe Asp Phe Met Glu Asn Ile Ser Leu Glu Gly Lys Thr Asn Phe Phe					

981	990	999	1008	1017	1026
GAG AAA CGA GTT TCA GAG TAT CAG CGT TTT GCA GTT ATG GCA GAA ACC ACA GAT					

Glu Lys Arg Val Ser Glu Tyr Gln Arg Phe Ala Val Met Ala Glu Thr Thr Asp					

1035	1044	1053
AAC GTC TTC ACC TTG GAT GCA GAT TTT 3'		

Asn Val Phe Thr Leu Asp Ala Asp Phe		

FIG. 3

Lipman-Pearson Protein Alignment

Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

Seq1 (1>351)	Seq2 (1>389)	Similarity
Tp53r2h. pro	R2. pro	Index
(15>351)	(53>389)	80.4
(1>351)	(39>389)	77.5

	10	20	30	40	50	60	70	80																																																																							
TP53R2H	M	G	D	P	E	P	E	A	A	G	L	Q	D	E	R	S	S	S	D	T	N	E	S	E	I	K	S	N	E	E	P	L	L	R	K	S	S	R	R	F	V	I	F	P	I	Q	Y	P	D	I	W	K	M	Y	K	Q	A	Q	A	S	F	W	T	A	E	E	V	D	L	S	K	D	L	P	H	W	N	K	
R2	G	T	R	V	L	A	S	K	T	A	R	R	I	F	Q	E	P	T	E	P	K	T	A	A	A	P	G	V	E	D	E	P	L	L	R	E	N	P	R	R	F	V	I	F	P	I	E	Y	H	D	I	W	Q	M	Y	K	K	A	E	A	S	F	W	T	A	E	E	V	D	L	S	K	D	I	Q	H	W	E	S
	40	50	60	70	80	90	100	110																																																																							

	90	100	110	120	130	140	150	160																																																																							
TP53R2H	L	K	A	D	E	K	Y	F	I	S	H	I	L	A	F	F	A	A	S	D	G	I	V	N	E	N	L	V	E	R	F	S	Q	E	V	Q	V	P	E	A	R	C	F	Y	G	F	Q	I	L	I	E	N	V	H	S	E	N	Y	S	L	L	I	D	T	Y	I	R	D	P	K	K	R	E	F	L	N	A	I	E
R2	L	K	P	E	E	R	Y	F	I	S	H	V	L	A	F	F	A	A	S	D	G	I	V	N	E	N	L	V	E	R	F	S	Q	E	V	Q	I	T	E	A	R	C	F	Y	G	F	Q	I	A	M	E	N	I	H	S	E	N	Y	S	L	L	I	D	T	Y	I	K	D	P	K	R	E	F	L	N	A	I	E	
	120	130	140	150	160	170	180	190																																																																							

	170	180	190	200	210	220	230	240																																																																							
TP53R2H	T	M	P	Y	V	K	K	K	A	D	W	A	L	R	W	I	A	D	R	K	S	T	F	G	E	R	V	V	A	F	A	A	E	G	V	F	F	S	G	S	F	A	A	I	F	W	L	K	K	R	G	L	M	P	G	L	T	F	S	N	E	L	I	S	R	D	E	G	L	H	C	D	F	A	C	L	M	F	Q
R2	T	M	P	C	V	K	K	K	A	D	W	A	L	R	W	I	G	D	K	E	A	T	Y	G	E	R	V	V	A	F	A	A	E	G	I	F	F	S	G	S	F	A	S	I	F	W	L	K	K	R	G	L	M	P	G	L	T	F	S	N	E	L	I	S	R	D	E	G	L	H	C	D	F	A	C	L	M	F	K
	200	210	220	230	240	250	260	270																																																																							

	250	260	270	280	290	300	310	320																																																																								
TP53R2H	Y	L	V	N	K	P	S	E	E	R	V	R	E	I	I	V	D	A	V	K	I	E	Q	E	F	L	T	E	A	L	P	V	G	L	I	G	M	N	C	I	L	M	K	Q	Y	I	E	F	V	A	D	R	L	L	V	E	L	G	F	S	K	V	F	Q	A	E	N	P	F	D	F	M	E	N	I	S	L	E	G	K
R2	H	L	V	H	K	P	S	E	E	R	V	R	E	I	I	N	A	V	R	I	E	Q	E	F	L	T	E	A	L	P	V	K	L	I	G	M	N	C	T	L	M	K	Q	Y	I	E	F	V	A	D	R	L	M	L	E	L	G	F	S	K	V	F	R	V	E	N	P	F	D	F	M	E	N	I	S	L	E	G	K	
	280	290	300	310	320	330	340	350																																																																								

	330	340	350																												
TP53R2H	T	N	F	F	E	K	R	V	S	E	Y	Q	R	F	A	V	M	A	E	T	T	O	N	V	T	L	D	A	D	F	
R2	T	N	F	F	E	K	R	V	G	E	Y	Q	R	M	G	V	M	S	S	P	T	E	N	S	F	T	L	D	A	D	F
	360	370	380																												

FIG. 4

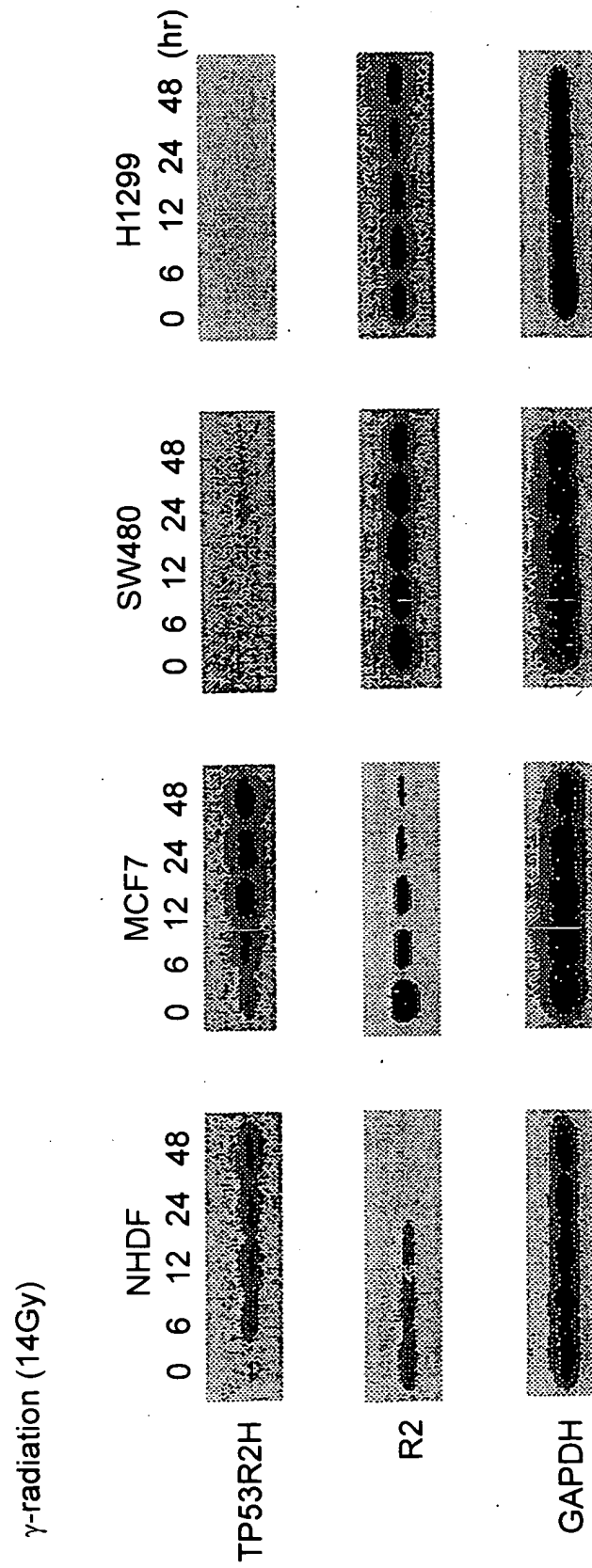


FIG. 5

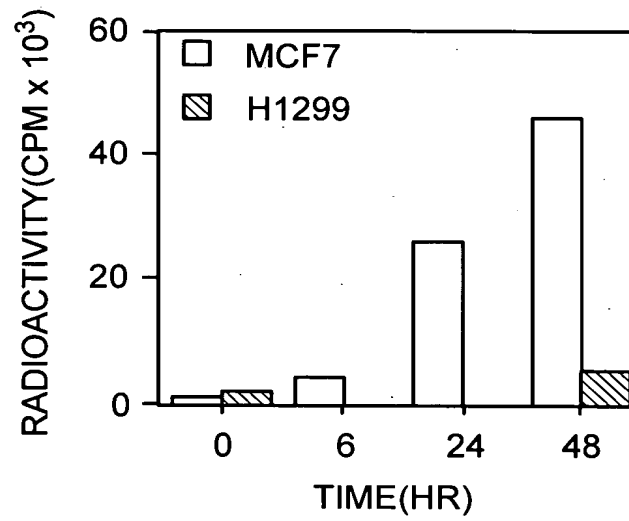


FIG. 6

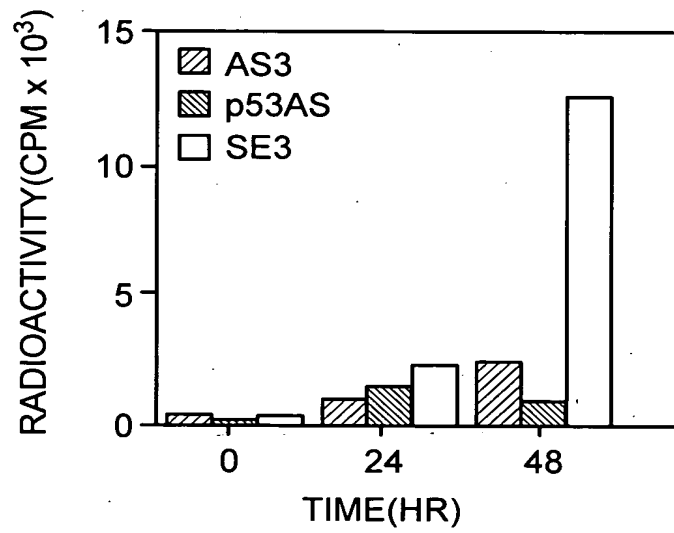


FIG. 7

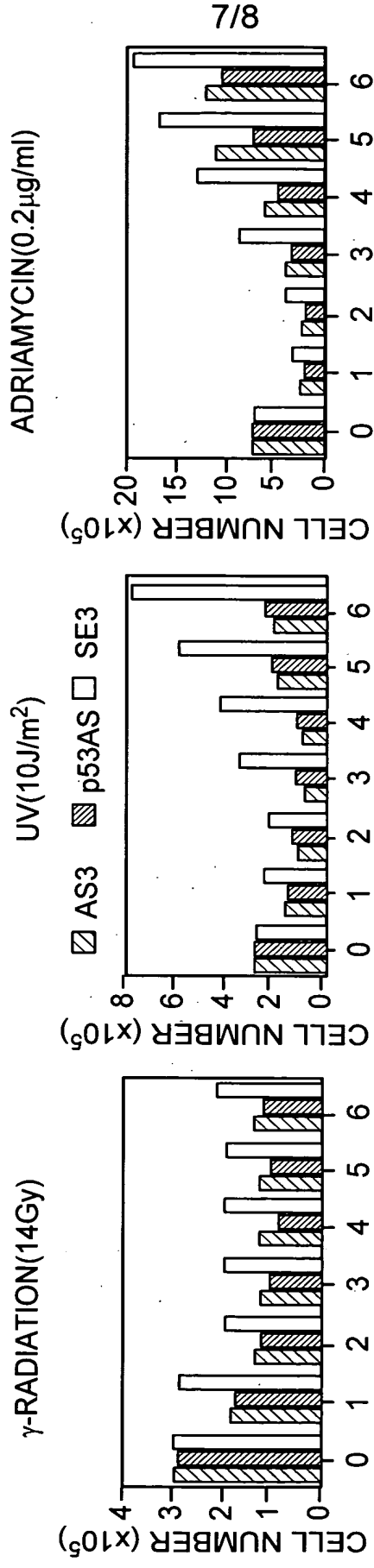
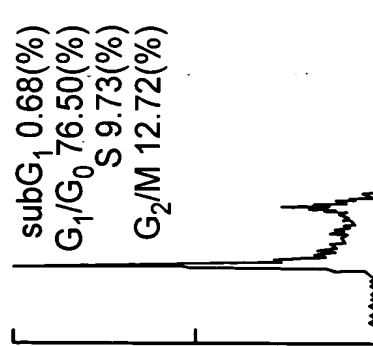


FIG. 8C

FIG. 8B

FIG. 8A

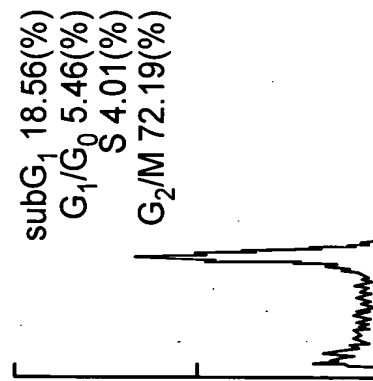
TP53R2H



ADRIAMYCIN(0HR)

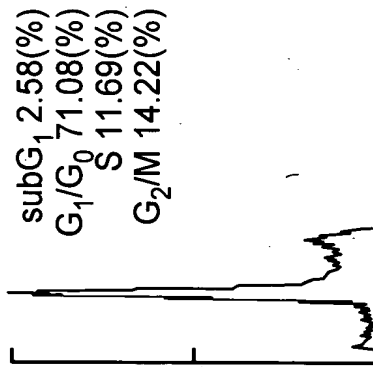
FIG. 9A

pcDNA3.1(+)



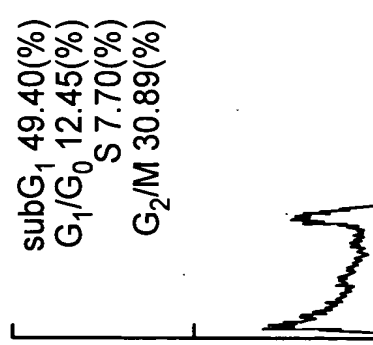
ADRIAMYCIN(48HR)

FIG. 9B



ADRIAMYCIN(0HR)

FIG. 9C



ADRIAMYCIN(48HR)

FIG. 9D